

Figure 1

M	G	T	P	A	Q	I	L	G	F
ATG	GGG	GCC	CCT	GCT	CAG	ATT	CTT	GGG	TTC
L	L	L	L	F	P	G	T	R	C
TTG	TTG	CTC	TTG	TTT	CCA	GGT	ACC	AGA	TGT

(leader, -20-1)

D	I	Q	M	T	Q	S	P	S	S
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC
L	S	A	S	L	G	Q	R	V	S
TTA	TCT	GCC	TCT	CTG	GGA	CAA	AGA	GTC	AGT
L	T	C							
CTC	ACT	TGT							

(fr.1, 1-23)

R	A	S	Q	D	I	G	I	N	L
CGG	GCA	AGT	CAG	GAC	ATT	GGT	ATT	AAC	TTA
H									
CAT									

(cdr1, 24-34)

T	L	Q	Q	E	P	D	G	T	I
TGG	CTT	CAG	CAG	GAA	CCA	GAT	GGA	ACT	ATT
K	R	L	I	Y					
AAA	CGC	CTG	ATC	TAC					

(fr2., 35-49)

A	T	S	S	L	G	S			
GCC	ACA	TCC	AGT	TTA	GGT	TCT			

(cdr2, 50-56)

G	V	P	K	R	F	S	G	S	R
GGT	GTC	CCC	AAA	AGG	TTC	AGT	GGC	AGT	AGG
S	G	S	D	Y	S	L	T	I	S
TCT	GGG	TCA	GAT	TAT	TCT	CTC	ACC	ATC	AGC
S	L	E	S	G	D	F	V	A	Y
AGC	CTT	GAG	TCT	GAA	GAT	TTT	GTA	GCC	TAT
Y	C								
TAC	TGT								

(fr3, 57-88)

L	Q	Y	A	S	S	P	Y	T	
CTA	CAA	TAT	GCT	AGT	TCT	CCG	TAC	ACG	

(cdr3, 89-97)

F	G	G	G	T	K	L	E	I	K
TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATA	AAA

(fr4, 98-107)

R	A	D	A	A	P	T	V	S	I
CGG	GCT	GAT	GCT	GCA	CCA	ACT	GTA	TCC	ATC
F	P	P	S	S	K	L	G		
TTC	CCA	CCA	TCC	AGT	AAG	CTT	GGG		

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Figure 2

M E C S W V F L F L L S I T T G V
 ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT GTC
 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu ser Ile Thr Thr Gly Val

H S
 CAC TCC
 His Ser (leader)

Q A Y L Q Q S G A E L V R S
 CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG TCT
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val arg Ser

G A S V K M S C K A S G Y T L T
 GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG ACC
 Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr leu Thr
 (1-30, Fr. #1)

S Y N M H
 AGT TAC AAT ATG CAC
 Ser Tyr Asn Met His (31-35, CDR 1)

W V K Q T P G Q G L E W I G
 TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG GAA TGG ATT GGA
 Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly

(36-49, Fr. #2)

N I F P G N G D T Y Y N Q K F K G
 AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT CAG AAG TTT AAG GGC
 Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn Gln Lys Phe Lys Gly
 (50-66, CDR 2)

K A S L T A D T S S S T A Y M Q
 AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC ACA GCC TAC ATG CAG
 Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln

I S S L T S E D S A V Y F C A R
 ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC TAT TTC TGT GCA AGA
 Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg

(67-98, Fr. # 3)

G N W E G A L D Y
 GGG AAC TGG GAG GGT GCT CTG GAC TAC
 Gly Asn Trp Glu Gly Ala Leu Asp Tyr

(99-107, CDR 3)

W G Q G T S V T V S S
 TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser

(108-118, Fr. # 4)

A K T T P P P V Y P L V P G S L
 GCC AAA ACG ACA CCC CCA CCC GTC TAT CCA CTG GTC CCT GGA AGC TTG GG
 Ala Lys Thr Thr Pro Pro Pro Val Tyr Pro Leu Val Pro Gly Ser Leu

(constant region)

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Figure 3A

DIQMTQSPSSLSASLGQRVSLTC — Framework #1, 1–23

RASQDIGINLH — CDR-1, 24–34

TLQQEPDGTIKRLIY — Framework #2, 35–49

ATSSLGS — CDR-2, 50–56

GVPKRFSGSRSGSDYSLTISLES^QGDFVAYYC — Framework #3, 57–88

LQYASSPYT — CDR-3, 89–97

FGGGTKLEIK — Framework #4, 98–107

96E72T" 05E99Z80

Figure 3B

QAYLQQSGAELVRSGASVKMSCKASGYTLT — Framework #1, 1-30

SYNMH — CDR-1, 31-35

WVKQTPGQGLEWIG — Framework #2, 36-49

NIFPGNGDTYYNQKFKG — CDR-2, 50-66

KASLTADTSSSTAYMQISLTSEDSAVYFCAR — Framework #3, 67-98

GNWEGALDY — CDR-3, 99-107

WGQGTSVTVSS — Framework #4, 108-118

08/766350-121396

Figure 4A

>gb|L41880|MUSIKCC Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.

```

67 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126
127 CTCACCTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 186
187 GATGGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 246
247 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 306
307 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGG 366
367 GGCACCAAGCTGGAAATAAAA 387

```

>gb|L48667|MUSX Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA antibody light chain mRNA.

```

1 GANATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 120
121 GATGGAACCTTTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 180
181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTGTCCGTACACGTTCCGGAGGG 300
301 GGCACCAAGCTGGAAATAAAA 321

```

>gb|J00565|MUSIGKAC1 Mouse ig kappa active gene: vk41 v-j region.

```

313 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 372
373 CTCACCTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 432
433 GATGGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 492
493 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 552
553 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 612
613 GGCACCAAGCTGGAAATCAAA 633

```

>emb|V00808|MMIGK7 Part of the murine gene for kappa-immunoglobulin leader peptide and variable part (cell line MOPC41).

```

314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373
374 CTCACCTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 433
434 GATGGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 493
494 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 553
554 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 613
614 GGCACCAAGCTGGAAATCAAA 634

```

>gb|I03643|I03643 Sequence 4 from patent US 4642334.

```

1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 120
121 GATGGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAA 180
181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 300
301 GGCACCAAGCTGGAAATCAAA 321

```

>gb|M59920|MUSIGKAA3 Mouse IG germline chain mRNA V-J region, partial cds.

```

1 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTC 60
61 ACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACAGAC 120
121 GGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGG 180
181 TTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAA 240
241 GATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGGAGGC 300
301 ACCAAGCTGGAAATCAAA 318

```

08/766350-121396

>gb|M36246|MUSIGLAFA Mouse Ig kappa-chain mRNA V region, partial cds, from
hybridoma H220-23.

```

1 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCTGGGCAAGT 60
61 CAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACCTATTAAACGC 120
121 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTCACTGGCAGTAGG 180
181 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGACTAT 240
241 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCTGGAGGGGGACCAAGCTGNAATA 300
301 AAA 303

```

>emb|Z22118|MDIGKVBS M.domesticus IgK variable region.

```

1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACCTGTCTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 120
121 GATGGAACCTATTAAACGCCTGATCTACAGCACATCCACTTTAAATTCTGGTGTCCCCAAA 180
181 AGGTTCACTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCTGGAGGG 300
301 GGGACCAAACCTGGAAATAAAA 321

```

>gb|M64168|MUSIGKAFT Mouse Ig active kappa-chain mRNA V-region.

```

4 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCTGGGCAAGT 63
64 CAGGACATTGGTAATAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACCTATTAAACGC 123
124 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTCACTGGCAGTAGG 183
184 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAATCTGAAGATTTTGTAGTCTAT 243
244 TACTGTCTACAATATGCTAGTTATACGTACACGTTCTGGAGGGGGACCAAGTTGGAACCTA 303
304 AAA 306

```

>emb|X02177|MMIGGVJ1 M.musculus mRNA for IgG kappa light chain(partial)
Loop 1

```

42 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 101
102 CTCACCTGTCTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 161
162 GATGGAACCTATTAAACGCCTGATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCCAAA 221
222 AGGTTCACTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 281
282 GAAGATTTTGCAGACTATTACTGTCTACAATATCTTAGTTATCCGCTCACGTTCTGGTGCT 341
342 GGGACCAAGCTGGAGCTGAAA 362

```

Figure 4B

08766350-121396

>gb|L48668|MUSY Mus musculus (cell line C3H/F2-20) chromosome 12 anti-DNA antibody heavy chain mRNA.

```

1 CAGGCTTATNTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
295 ----- 311
312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357 .

```

>gb|L48680|MUSAL Mus musculus (cell line C3H/F2-3) chromosome 12 anti-DNA antibody heavy chain mRNA.

```

1 CAGGCTTATGTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACAGATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CGTAGACAGGGCCTGGAATGGATTGGAGCAATTTATCCAGGAAATGGTGATACTTCCTAT 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGATTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGAGA 298
299 GGGGTAACCTACGTAGGACATATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 357
358 TCA 360

```

>emb|X64805|MMAIDHCH M.musculus mRNA for anti-Id mAB 114 heavy chain, variable region.

```

1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTAAGGCCTGGGTCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAT 300
301 TACTCCGGTAGTATAGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 354

```

>gb|M17953|MUSIGHXW Mouse Ig rearranged H-chain V-region mRNA VJ1.

```

96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155
156 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215
216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 275
276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
393 ----- 427
428 CTGGGGCACAGGGACCACGGTCACCGTCTCC 458

```

>gb|I05921|I05921 Sequence 37 from patent EP 0274394.

```

96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155
156 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215
216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 275
276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
393 ----- 427
428 CTGGGGCACAGGGACCACGGTCACCGTCTC 457

```

Figure 5A

>emb|Z22117|MDIGGVBC M.domesticus IgG variable region.

```

2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATAT 61
62 CCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATGCACTGGGTGAAGCAGAAGC 121
122 CTGGGCAGGGCCTTGAGTGGATTGGAGAGATTTATCCTGGAAGTGGTAATACTTACTACA 181
182 ATGAGAAGTTCAAGGGYAAGGCCTCACTGACTGCAGACAAATCCTCCAGCACAGCCTACA 241
242 TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGACGTTACT 301
302 ----- 314
315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

```

>gb|M15224|MUSIGLAF Mouse IgM H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAG 295
296 ----- 314
315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

```

>gb|M15226|MUSIGLAH H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
295 ----- 317
318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

```

>gb|M15225|MUSIGLAG H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

1 CAGGTTTCAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60
61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
295 ----- 311
312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

```

>gb|M20835|MUSIGKCLP Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody.

```

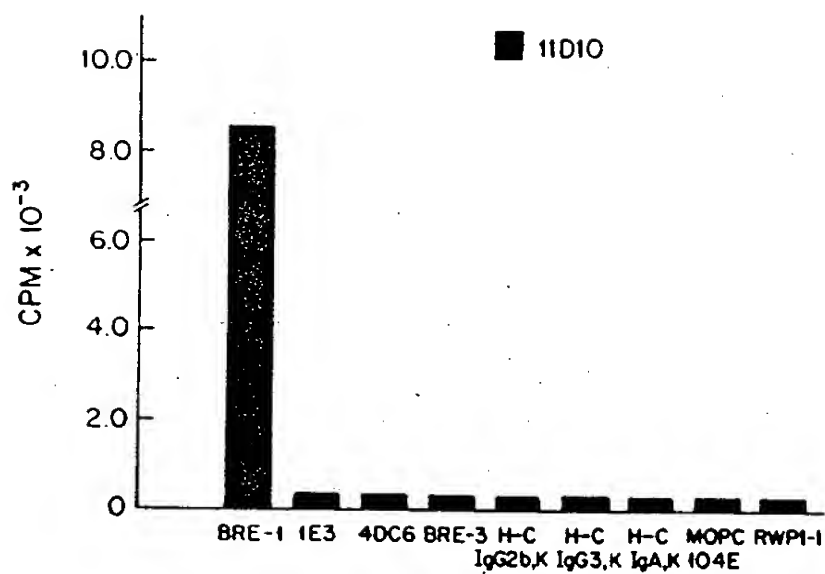
106 CAGGTCCAAGTGCAGCAGCCTGGTGCTGAGCTTGTGAAGCCTGGGGCCTCAGTGAAGCTG 165
166 TCCTGCAAGGCTTCTGGCTACACTTTCACCACTACTGGATAAACTGGGTGAAGCAGAGG 225
226 CCTGGACAAGGCCTTGAGTGGATTGGAAATATTTATCCTGGTAGTAGTACTAAGTAC 285
286 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACATCCTCCAGCACAGCCTAC 345
346 ATGCAGCTCAGCAGCCTGACATCTGACGACTCTGCGGTCTATTATTGTGCAAGACG 401
402 ----- 416
417 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 462

```

Figure 5B

08766350.121396

Figure 6



96E72T 05E99Z80

Figure 7

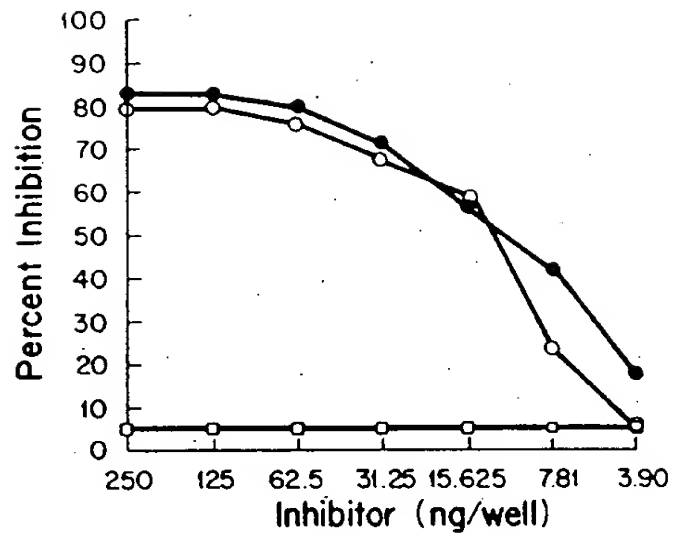


Figure 8

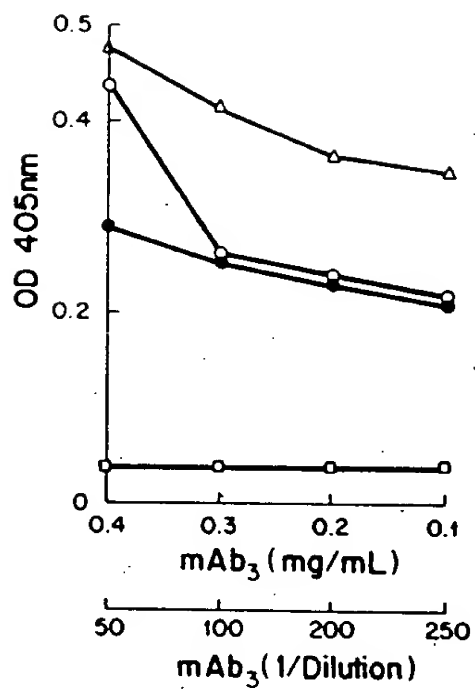
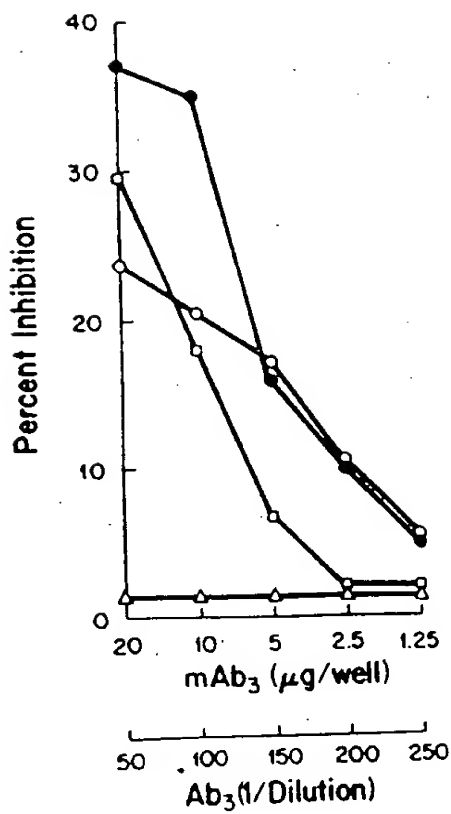
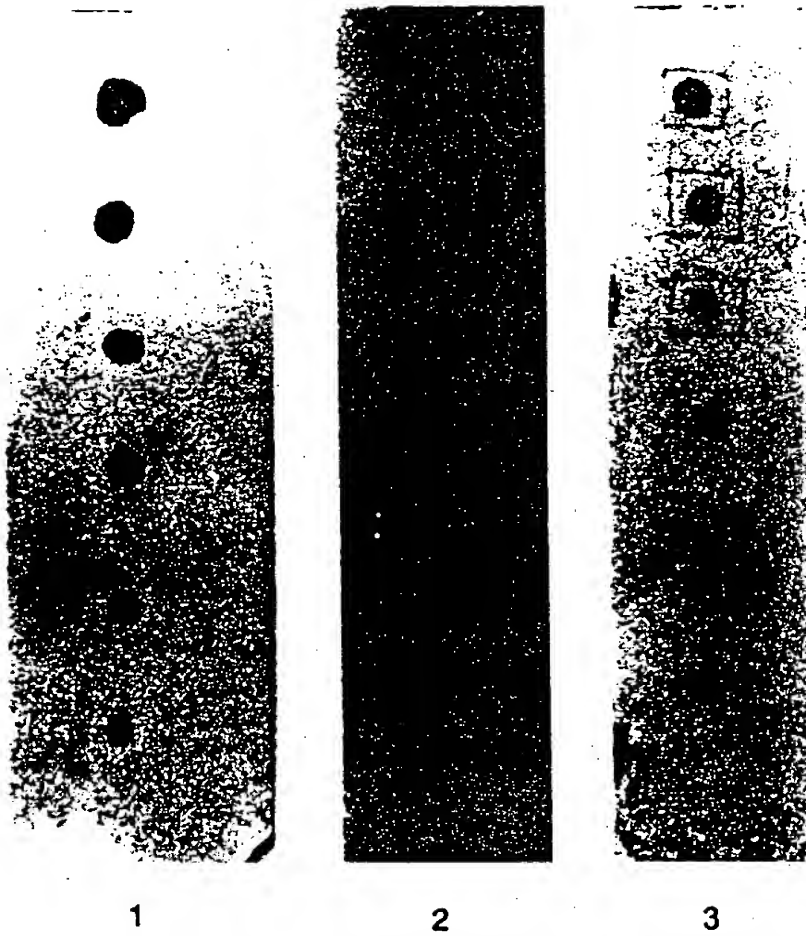


Figure 9



96ET2T*05E99480

Figure 10



08766350.121396

Figure 11

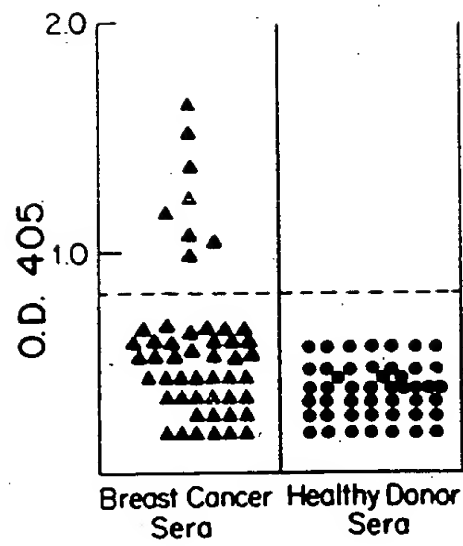


Figure 12

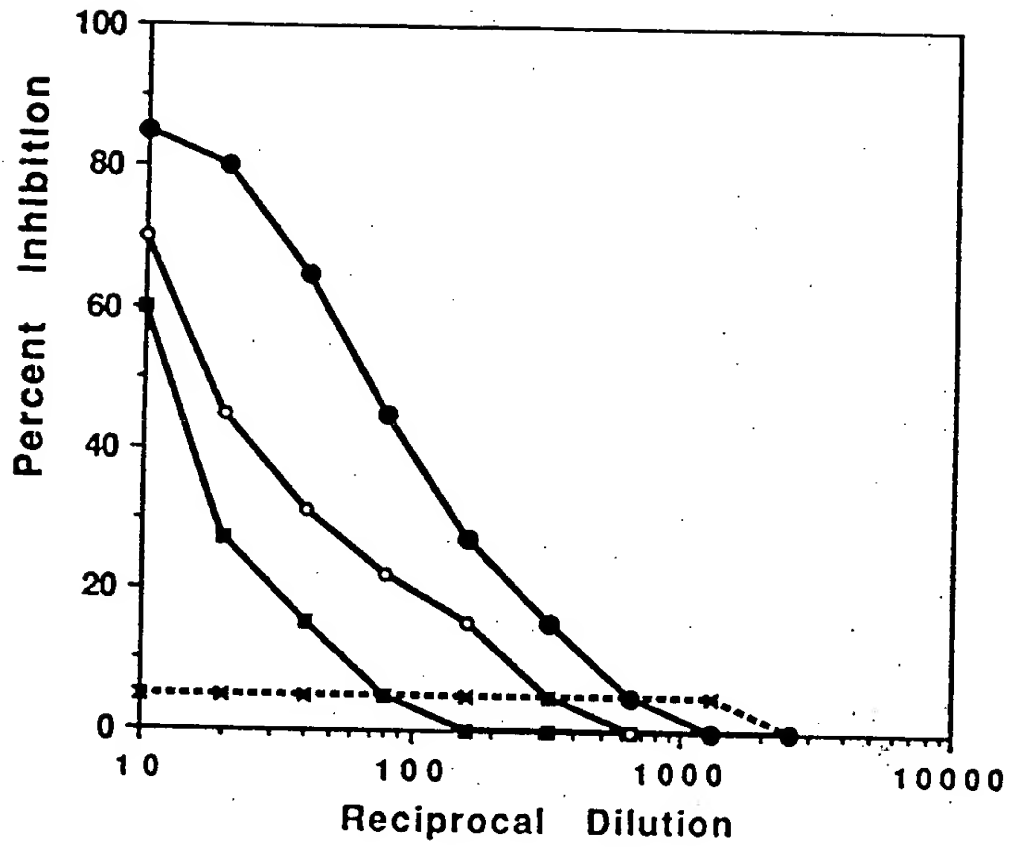
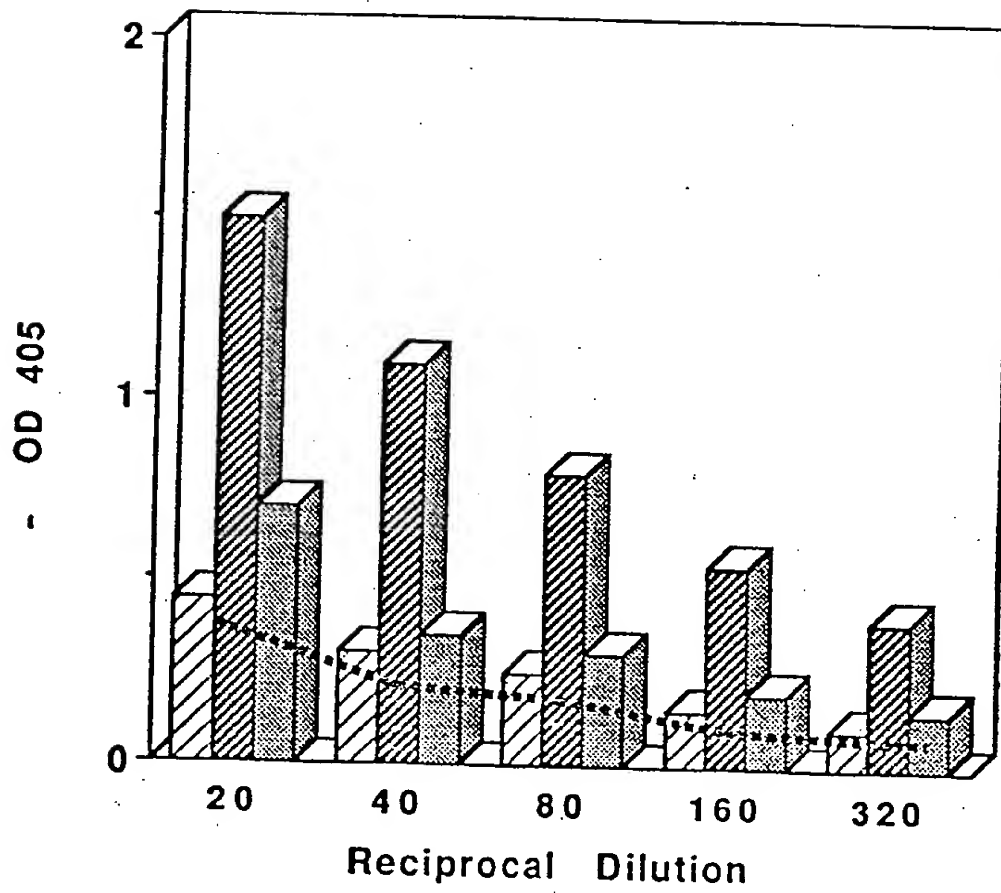
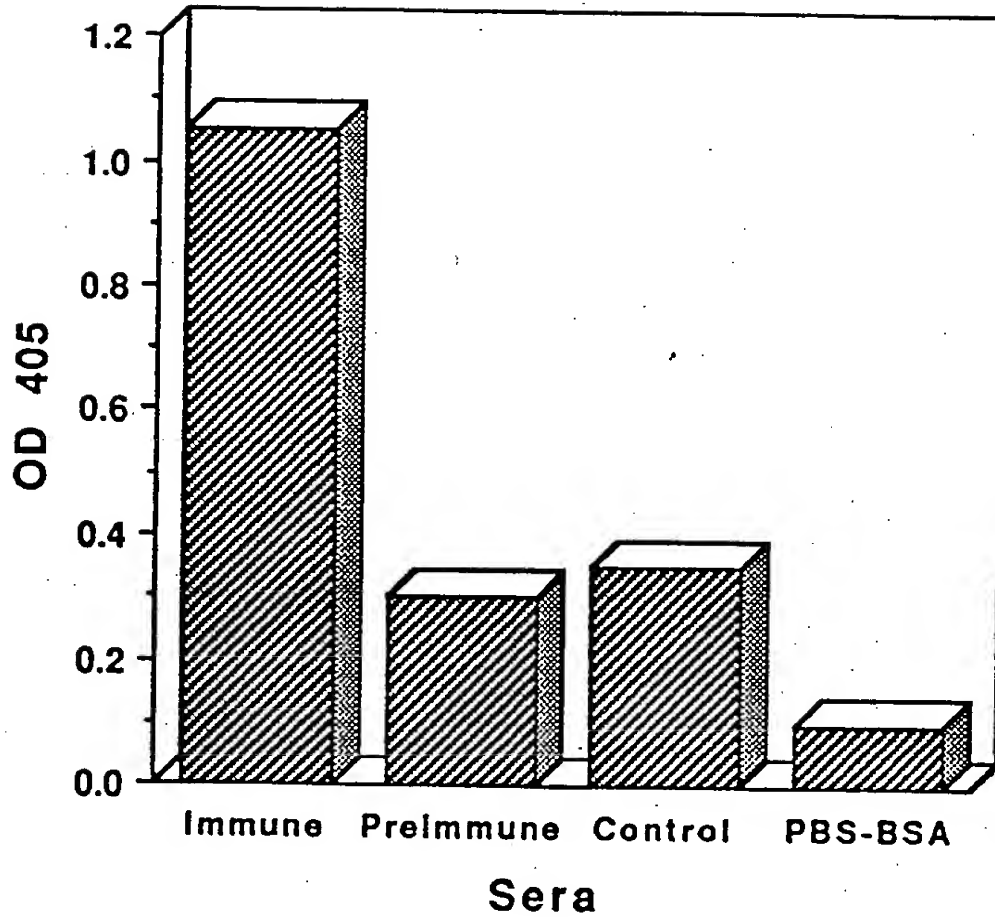


Figure 13



966121-05299780

Figure 14



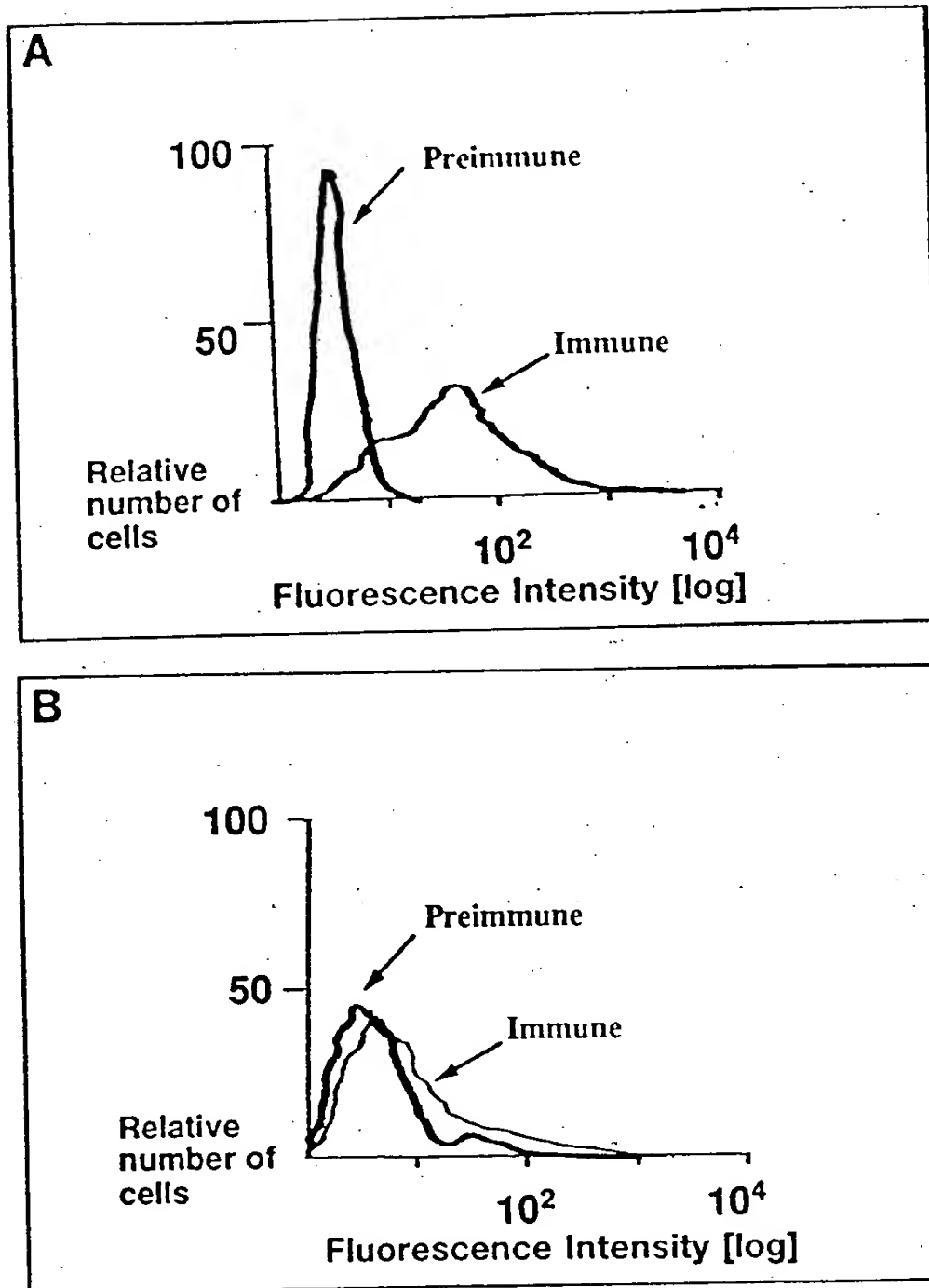


Figure 15

Figure 16

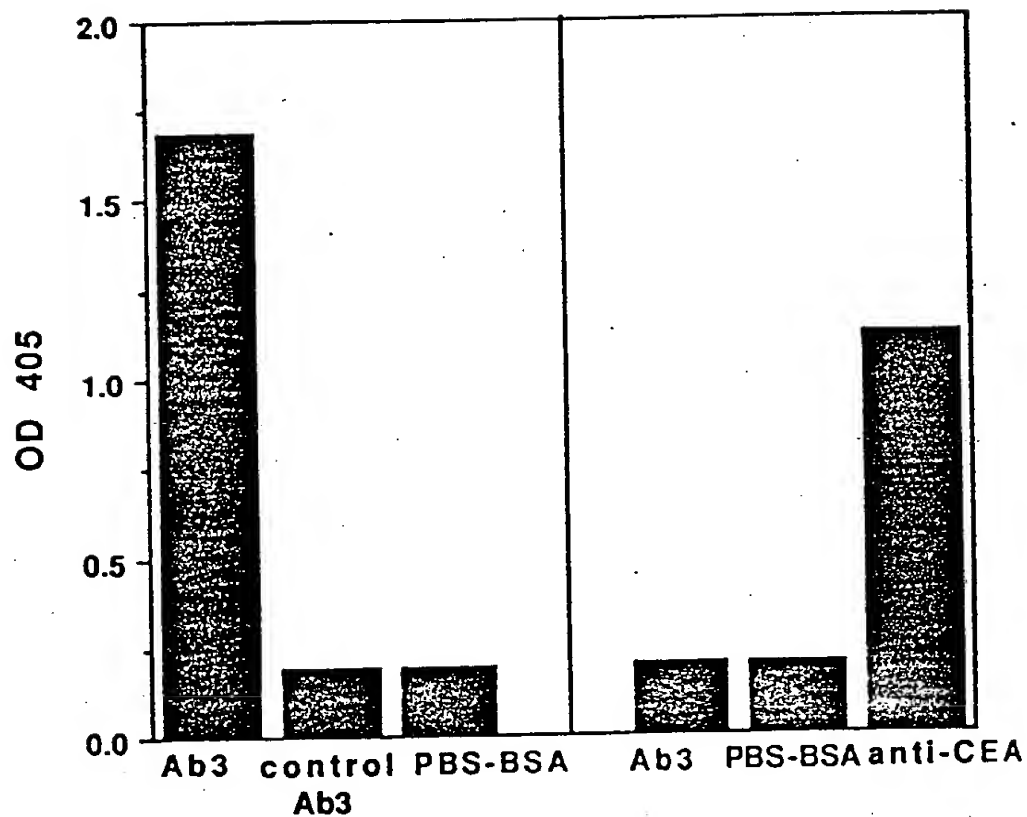


Figure 17

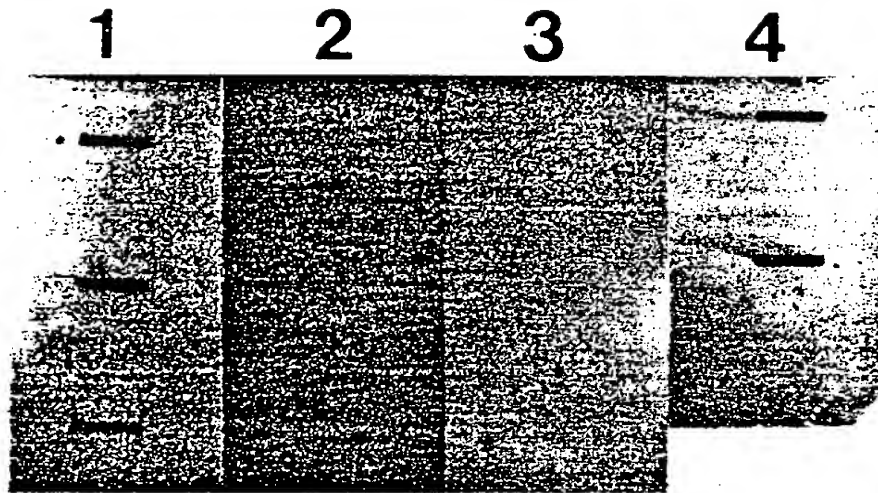
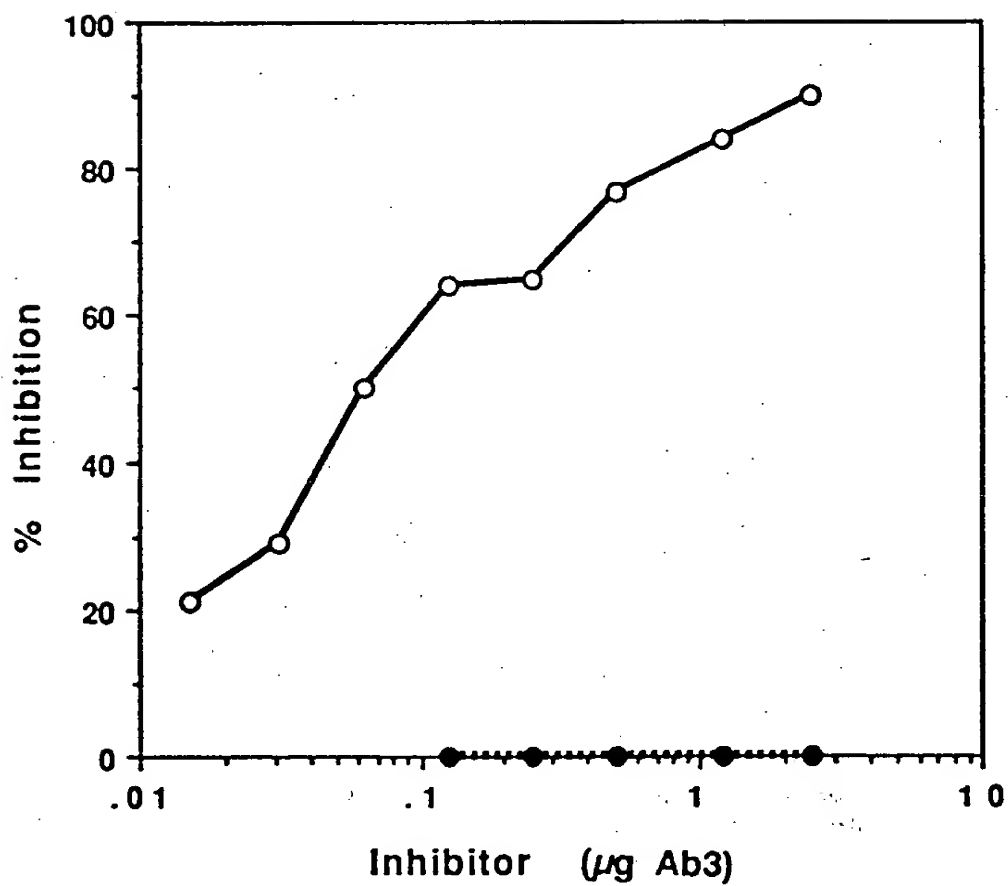
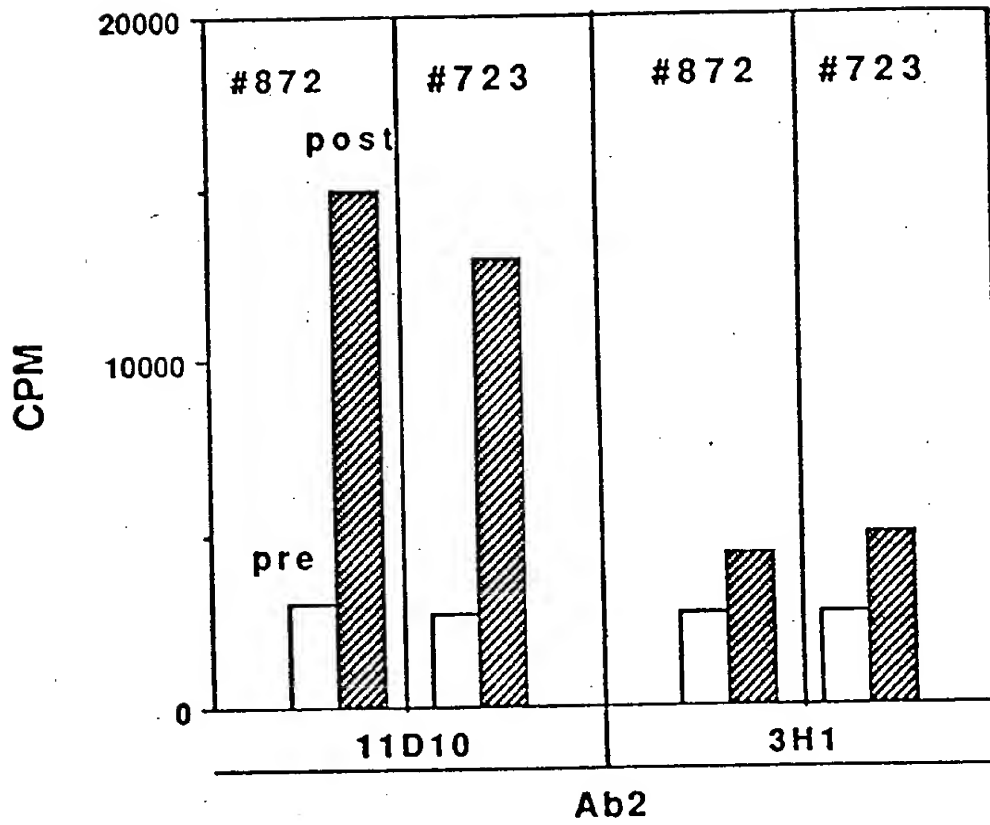


Figure 18



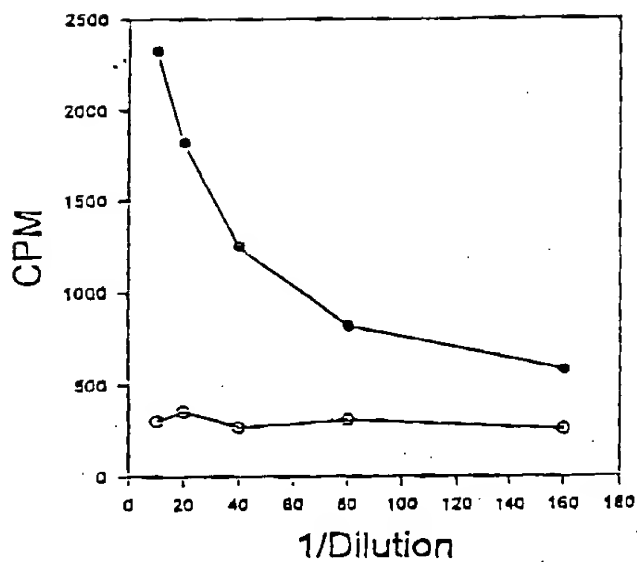
96ET2T"05E99Z80

Figure 19



96ET2T*05E99Z80

Figure 20



96E121-05E99280

Figure 21

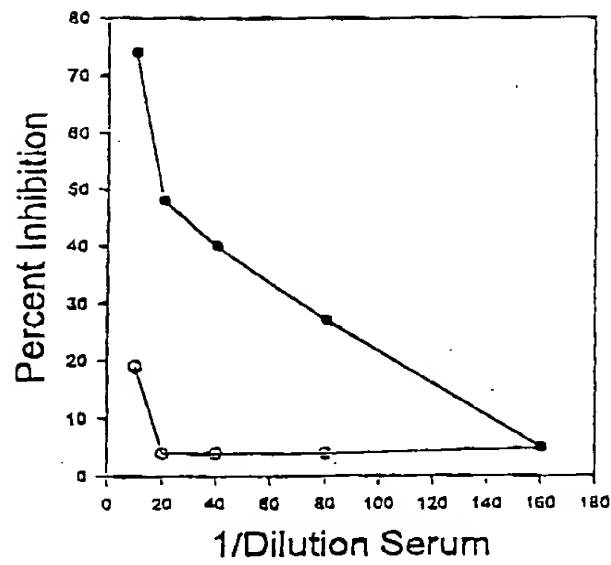


Figure 22

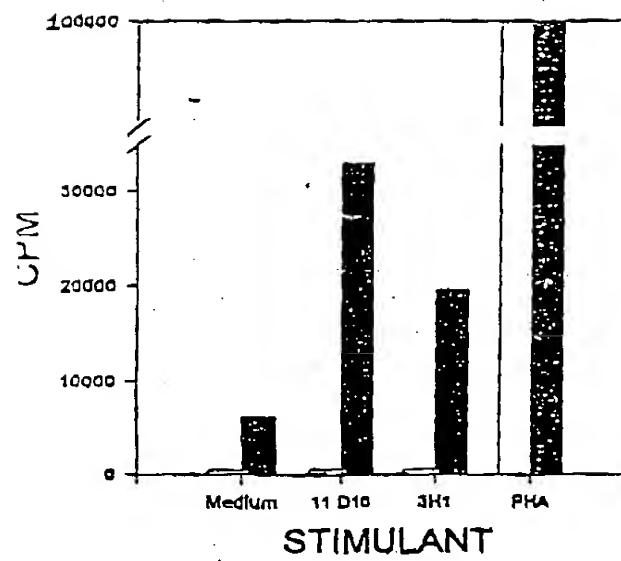


Figure 23

Alignment of 11D10 CDRs with HMFG Tandem Repeat

Q G L E W I G <u>N I F P G N G D T Y Y N O</u>	V _H (near CDR 2)
: : : : :	
G S T A P P A H G V T S A P D T R P A P	HMFG repeat (direct)
: : :	
D G T I K R L I Y <u>A T S S L G S</u> G V P L	V _L (near CDR 2)
P S E R P	
P A P R T D P A S T V G H A P P A T S G P A P	HMFG repeat (rev.)
: : : : : : : :	
H T L Q Q E P D G T I K R L I Y <u>A T S S L G S</u>	V _L (near CDR 2)
: : : :	
A Y Y C L O Y A S S P Y T F G G G T K L E I K	V _L (near CDR 3)

96ET2T-05E99Z80

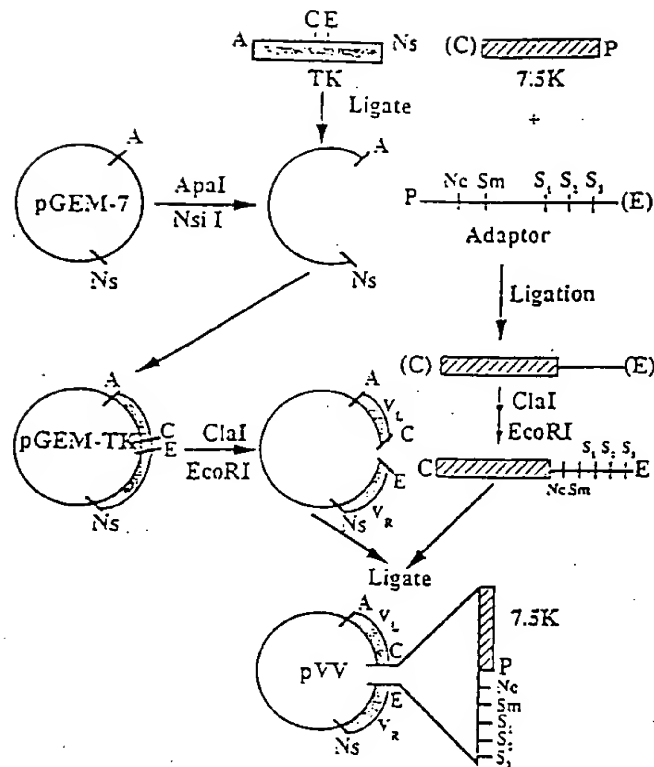


Figure 24

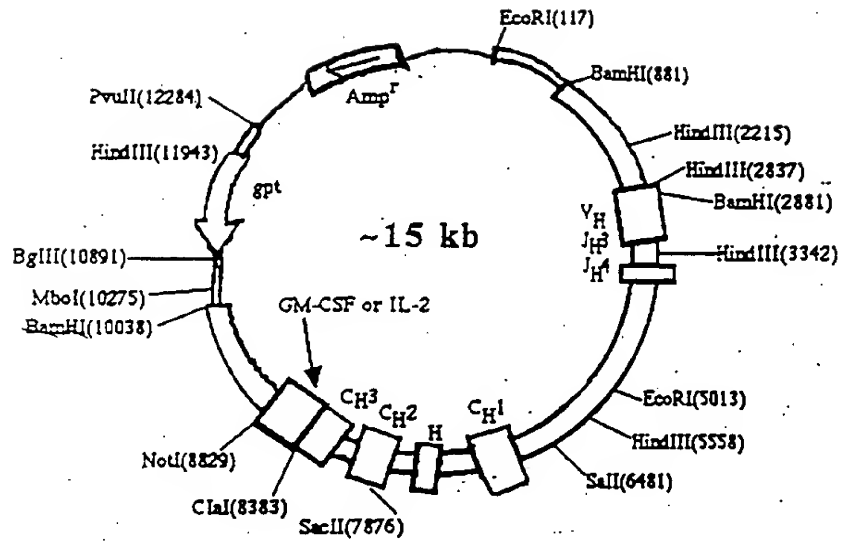


Figure 25A

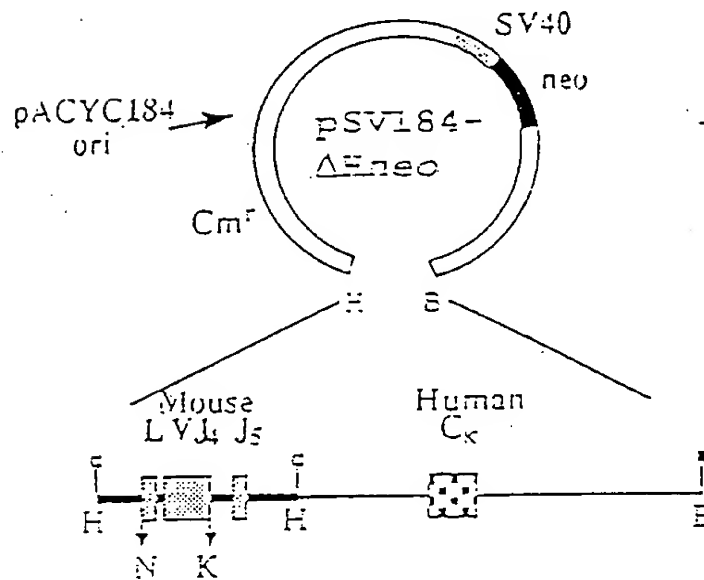


Figure 25B

Figure 26(A)

11D10: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60

1	23E.....SS.NW.....D.....	82
2	23E.....SS.NW.....D.....	82
3	23E.....SS.NW.....D.....	82
4	23E.....P.....SS.NW.....D.....	82
5	1E.....SS.NW.....D.....	60
6	1E.....SS.NW.....D.....	59
7	1E.....RS.NW.....D.....	60
8	1E.....E.SGY.SW...K.....S.T.N....	60
9	1E.....SS.NW.....D.....	54
10	1E.....E.SGY.SW...K.....A.T.D....	60
11	1	X.....E.....NS.NW.....D.....	55
12	1E...A....E.GY.SW...K.....A.T.D....	60
13	14E.....E.SGY.SW...K.....A.T.D....	73
14	1	EL.....E.....E.SGY.SW...K.....A.T.D....	60
15	2	ELVL.....E.....E.NGY.GW...K.....A.T.H....	61

11D10: 61 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIK 107

1	83D.....	129
2	83D.....W.....	129
3	83D.....W.....	129
4	83D.....W.....	129
5	61D.....W.....	106
6	60D.....W.....	106
7	61D.....T.W.....	106
8	61AD.....	107
9	55D.....X.....	107
10	60AD.....	106
11	56V.....YT.....L.....	102
12	61	..G.....AD.....Y.W.....	106
13	74AD.....L.Y.L...A....L.....	120
14	61AD.....Y.L...A....L.....	107
15	62AD.....Y.R.....	108

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Figure 26(B)

11D10: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGQGLEWIGNIFPGNGDTYY 60

1 1P.S.....F.....R.....A.Y.....S. 60
 2 20P.....F.....R.....A.Y.....S. 79
 3 1 EVQ....P...KP....I.....F.D.Y....K.....E.Y..S.N... 60
 4 1 .IQ....P...P....I.....F.D.YI....R..E.....W.Y..S.N.K. 60
 5 1 .VQ....P...KP....L.....F.D.TI....S.....W.Y..S.N.K. 60
 6 1 .VQ..E....KP....L.....F..W.....R.....K.N.S..R.N. 60
 7 20 .VQ.....AKP.....F.A.W.....R.....Y.N.NT.Y.E. 79
 8 1 EVQ.....KP....L.....F..W.....R.....E.D.SDSY... 60
 9 1 .VQ....E...A.P.....F.R.W.....R..A....A.Y...S..N. 60
 10 1 .VQ.....P.T...I.....F.N.WLG...R..H.....D.Y..G.Y.N. 60
 11 20 .VQ.....AKP.....F..R.....R.....Y.N.ST.Y.E. 79
 12 1 .VQ.....AKP.....F..W.....R.....Y.N.ST.Y.E. 60
 13 1 .IQ....P...P....I.....F.D.YI....R..E.....W.Y..S.N.K. 60
 14 1 .VQ.....P.T.....A...F.N.WIG...R..H.....D.Y..G.Y.N. 60
 15 1 EVQ....TV.A.P.....F..W.....R.....A.Y...S..R. 60

11D10: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG=NWEG=ALDYWGQGTSTVTSS 118

1 61T..V.K.....L.....=DYS.=SI.....TL.... 118
 2 80T..V.K.....L.....xxxxxxxxxx=xx.V..T..T.... 140
 3 61 .E.....K.....L.....xxxxxxxxxx=.M..... 120
 4 61 .E.....T..V.....L.....=xxx=.M..... 117
 5 61 .D.....TM...K.....L.....=VAR.S=.M..... 119
 6 61 .E...S..T..V.K.....L.....Y...xxxxxxxxxx.....T.... 123
 7 80 ..N..D..T...K.....L.....Y.T.xxx.Y..=.M..... 139
 8 61T..V.K.....F.....Y...xxxxxxxxxx=xM..... 120
 9 61K...V..A....EL...A.....Y...S=RYR.=SM..... 119
 10 61 .E.....T.....L.....P=HYY.=SG.....TL.... 118
 11 80D..T...K.....L...F.....Y...=x.=VF.....TL.... 135
 12 61D..T...K.....L.....L.Y...W=VYYY=.M..... 118
 13 61 .E.....T..V.....L.....=xxx=.M..... 117
 14 61 .E.....T.....L.....I.Y...P=FYFY=.M.....C.... 118
 15 61K...V..A....EL...N.....Y.T..=GLFT=.M..... 115

96ET2T" 05E99Z80

Figure 26(C)**Light Chain**

 VL consensus: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 60
 11D10: 1Q.....IN.HT.....G..... 60

HMFG fragments: GSIAPPAHRVISAPE\$RPPP
 ppprsepastvrhappatsg

 VL consensus: 61 RFSGSRSGSDYSLTISSLES GDFVDYYCLQYASSPYTFGGG TKLEIK 107
 11D10: 61A..... 107

HMFG fragments: ppprsepastvrhappatsg

Heavy Chain

 VH consensus: 1 QVQLQQSGAELVRPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGAIYPGNGDTNY 60
 11D10: 1 .AY.....S.....L...N.....T.....N.F.....Y. 60

HMFG fragments: APDTRPPP

 VH consensus: 61 NQKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARGxxxGAMDYWGQGT SVTVSS 118
 11D10: 61S.....I.....NWE..L..... 118

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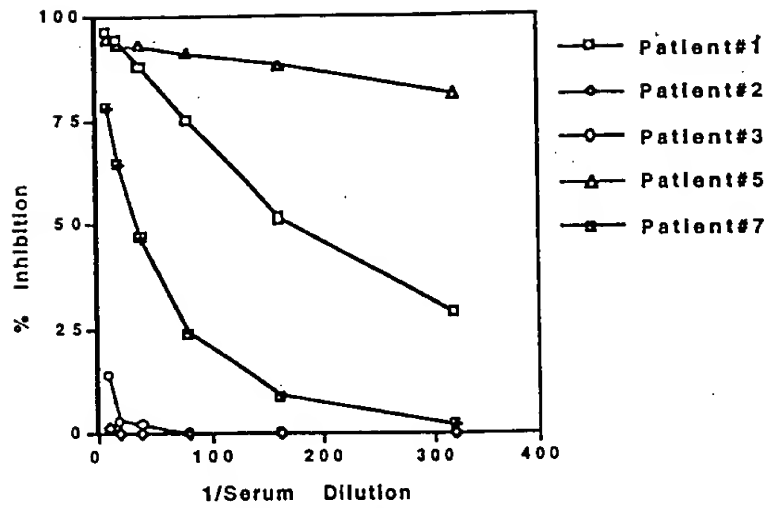


Figure 27A

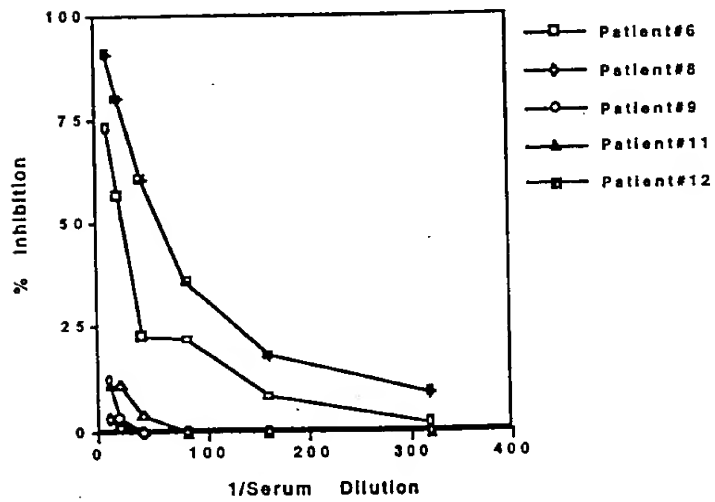


Figure 27B

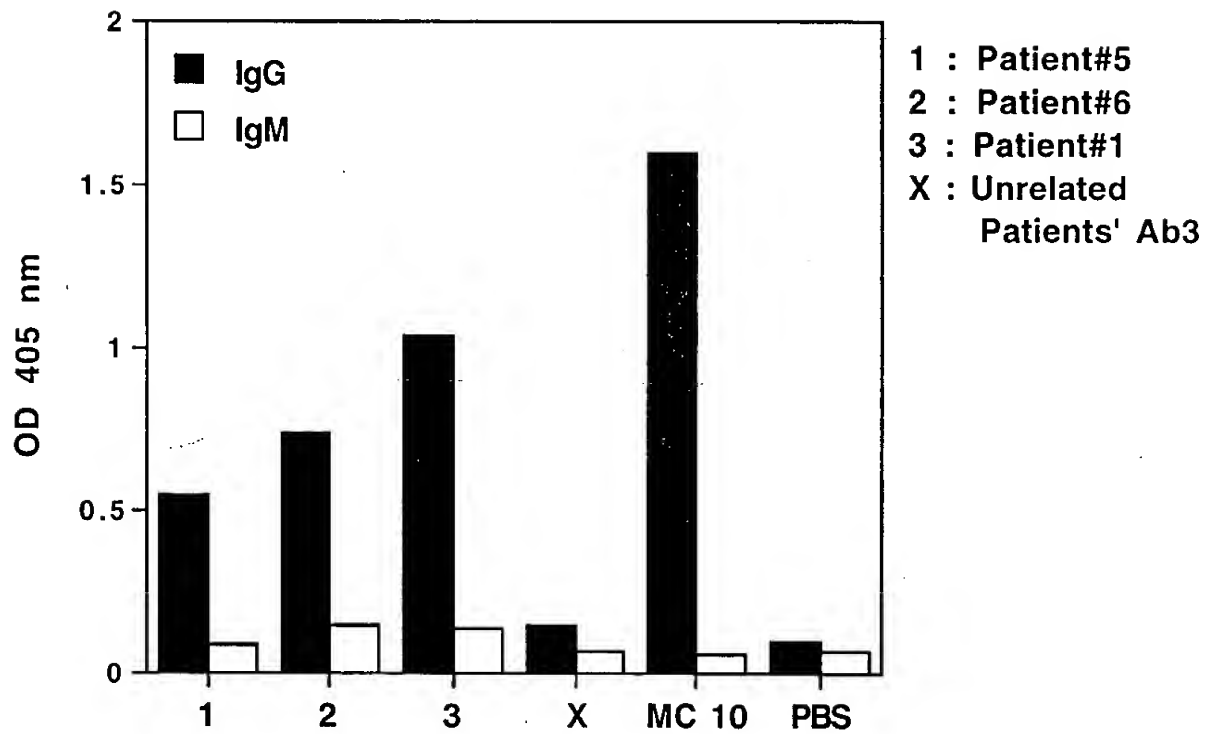


Figure 28

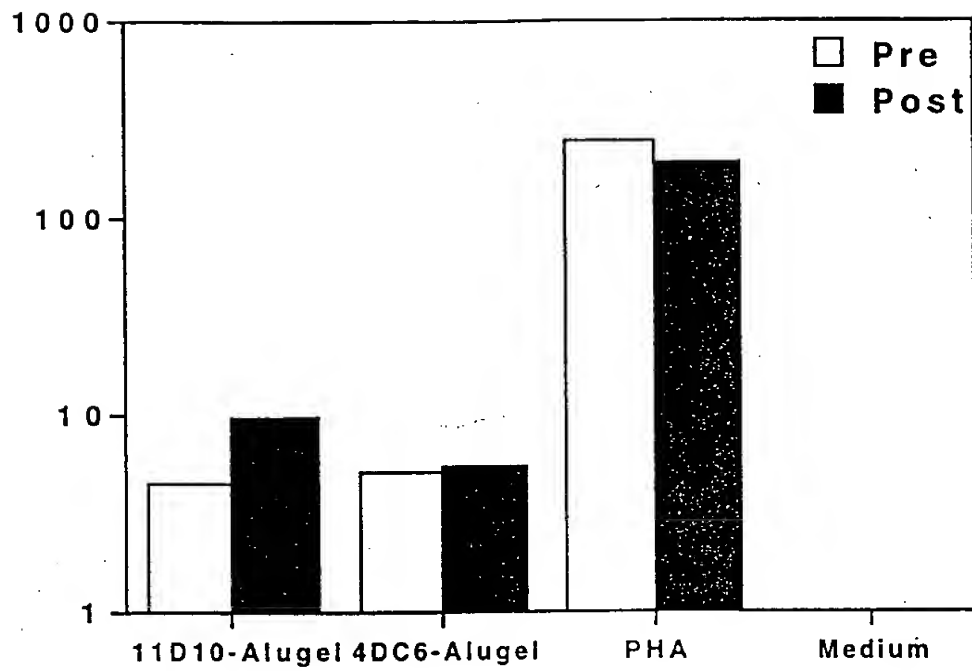


Figure 29 A

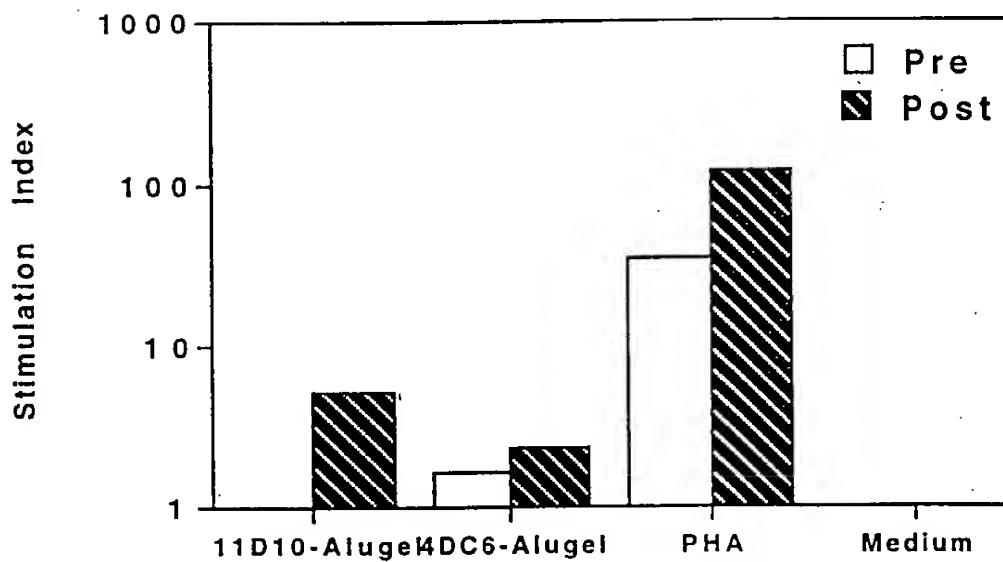


Figure 29B